Figure 1

bcl Consensus PCR Primers

```
                            Ile
EcoRI AspTrpGlyArgValValAla
5- AGATCTGAATTCAACTTGGGGGIC(A)GIA(G)TXGTXGC -3' bclx 1-32


      AspTrpGlyGlyGlnGluAsnAspGlnIleTrp
            AGGGTIGGIGGXACXAGA(G)ACA(T)(C)TAGGT
5'- AGATCT'AAGCTTGTCCCAICCICCXTGXTCC(T)TGA(G)ATCCA -3' bclX 2-39
```
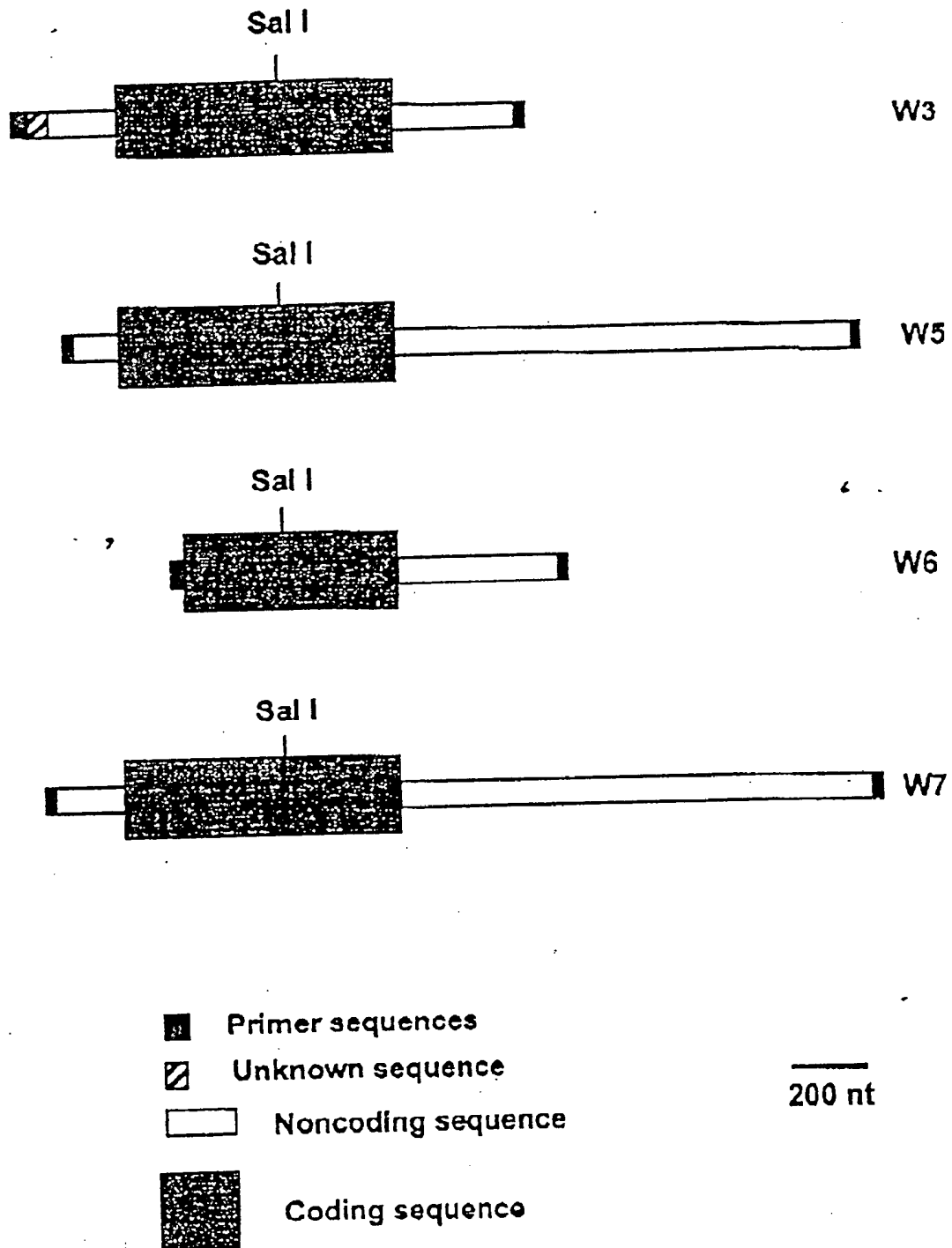
Figure 2

Cdi-1 cDNA clones

Sal I

W3

Sal I

W5

Sal I

W6

Sal I

W7

■ Primer sequences
▨ Unknown sequence
□ Noncoding sequence

■ Coding sequence

──── 200 nt

Figure 3

```
          10            20            30            40
          *             *             *             *
GAG GAT CTA CAG GGG ACA AGT AAA GGC TAC ATC CAG ATG CCG GGA ATG
CTC CTA GAT GTC CCC TGT TCA TTT CCG ATG TAG GTC TAC GGC CCT TAC


      >Aha2
        |
  50    |       60            70            80            90
  *     |       *             *             *             *
CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC CCA CTC AGC CCC TGG GAG
GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG GGT GAG TCG GGG ACC CTC


      100           110           120           130           140
       *             *             *             *             *
CAG CAG CCG CCA GCC CCT CGG ACC TCC ATC TCC ACC CTG CTG AGC CAC
GTC GTC GGC GGT CGG GGA GCC TGG AGG TAG AGG TGG GAC GAC TCG GTG


>Smal                >BamH1
  |                    |
  |      150           |160           170           180           190
  |       *            |  *            *             *             *
CCG GGT TGG GCC AGG ATC CCG GCA GGC TGA TCC CGT CCT CCA CTG AGA
GGC CCA ACC CGG TCC TAG GGC CGT CCG ACT AGG GCA GGA GGT GAC TCT


      200           210           220           230           240
       *             *             *             *             *
CCT GAA AA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC
GGA CTT TT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG
         ?     M   A   S   G   Q   G   P   G   P   P   R   Q   E   C>


      250           260           270           280           290
       *             *             *             *             *
GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC
CCT CTC GGA CGG GAC GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG
     G   E   P   A   L   P   S   A   S   E   E   Q   V   A   Q   D>


      300           310           320           330
       *             *             *             *
ACA CAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC CAT CAG CAG GAA
TGT CTC CTC CAA AAG GCG TCG ATG CAA AAA ATG GCG GTA GTC GTC CTT
  T   E   E   V   F   R   S   Y   V   F   Y   R   H   Q   Q   E>


340           350           360           370           380
 *             *             *             *             *
CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA GAG ATG GTC ACC
GTC CTC CGA CTT CCC CAC CGA CGG GGA CGG CTG GGT CTC TAC CAG TGG
  Q   E   A   E   G   V   A   A   P   A   D   P   E   M   V   T>


                        >Ncol
                          |
390           400         |410           420           430
 *             *          | *             *             *
TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC
AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG
  L   P   L   Q   P   S   S   T   M   G   Q   V   G   R   Q   L>


      440           450           460           470           480
       *             *             *             *             *
GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG
CGG TAG TAG CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC
```

Figure 3 cont.

```
        A    I    I    G    D    D    I    N    R    R    Y    D    S    E    F    Q>

                                   >Pst1
                                      |
        490            500            |510            520            530
         *              *             |  *              *              *
    ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC
    TGG TAC AAC GTC GTG GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG
     T   M   L   Q   H   L   Q   P   T   A   E   N   A   Y   E   Y>

            540            550            560            570
             *              *              *              *
    TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC ATC AAT TGG GGC
    AAG TGG TTC TAA CGG TGG TCG GAC AAA CTC TCA CCG TAG TTA ACC CCG
     F   T   K   I   A   T   S   L   F   E   S   G   I   N   W   G>

    580            590            600            610            620
     *              *              *              *              *
    CGT GTG GTG GCT CTT CTG GGC TTC GGC TAC CGT CTG GCC CTA CAC GTC
    GCA CAC CAC CGA GAA GAC CCG AAG CCG ATG GCA GAC CGG GAT GTG CAG
     R   V   V   A   L   L   G   F   G   Y   R   L   A   L   H   V>

        630            640            650            660            670
         *              *              *              *              *
    TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG ACC CGC TTC GTG
    ATG GTC GTA CCG GAC TGA CCG AAG GAT CCG GTC CAC TGG GCG AAG CAC
     Y   Q   H   G   L   T   G   F   L   G   Q   V   T   R   F   V>

>Sal1
|
        680            690            700            710            720
         *              *              *              *              *
    GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG
    CAG CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC
     V   D   F   M   L   H   H   C   I   A   R   W   I   A   Q   R>

            730            740            750            760            770
             *              *              *              *              *
    GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC
    CCA CCG ACC CAC CGT CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG
     G   G   W   V   A   A   L   N   L   G   N   G   P   I   L   N>

            780            790            800            810
             *              *              *              *
    GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA
    CAC GAC CAC CAA GAC CCA CAC CAA GAC AAC CCG GTC AAA CAC CAT GCT
     V   L   V   V   L   G   V   V   L   L   G   Q   F   V   V   R>

    820            830            840            850            860
     *              *              *              *              *
    AGA TTC TTC AAA TCA TGA C TCC CAA GGG TGC CCT TTG GGT CCC GGT TCA
    TCT AAG AAG TTT AGT ACT G AGG GTT CCC ACG GGA AAC CCA GGG CCA AGT
     R   F   F   K   S   *>

                        >Afl2
                           |
    870            880    |    890            900            910
     *              *     |      *              *              *
    GAC CCC TGC CTG GAC TTA AGC GAA GTC TTT GCC TTC TCT GTT CCC TTG
    CTG GGG ACG GAC CTG AAT TCG CTT CAG AAA CGG AAG AGA CAA GGG AAC

                        >Hind3
```

Figure 3 cont.

```
          920           930           940           950           960
           *             *             *             *             *
   CAG GGT CCC CCC TCA AGA GTA CAG AAG CTT TAG CAA GTG TGC ACT CCA
   GTC CCA GGG GGG AGT TCT CAT GTC TTC GAA ATC GTT CAC ACG TGA GGT

                                                       >PstI
                                                         |
          970           980           990          1000          1010
           *             *             *             *             *
   GCT TCG GAG GCC CTG CGT GGG GGC CAG TCA GGC TGC AGA GGC ACC TCA
   CGA AGC CTC CGG GAC GCA CCC CCG GTC AGT CCG ACG TCT CCG TGG AGT

                                              >ApaI
                                                |
         1020          1030          1040        | 1050
           *             *             *         |  *
   ACA TTG CAT GGT GCT AGT GCC CTC TCT CTG GGC CCA GGG CTG TGG CCG
   TGT AAC GTA CCA CGA TCA CGG GAG AGA GAC CCG GGT CCC GAC ACC GGC

         1060          1070          1080          1090          1100
           *             *             *             *             *
   TCT CCT CCC TCA GCT CTC TGG GAC CTC CTT AGC CCT GTC TGC TAG GCG
   AGA GGA GGG AGT CGA GAG ACC CTG GAG GAA TCG GGA CAG ACG ATC CGC

         1110          1120          1130          1140          1150
           *             *             *             *             *
   CTG GGG AGA CTG ATA ACT TGG GGA GGC AAG AGA CTG GGA GCC ACT TCT
   GAC CCC TCT GAC TAT TGA ACC CCT CCG TTC TCT GAC CCT CGG TGA AGA

         1160          1170          1180          1190          1200
           *             *             *             *             *
   CCC CAG AAA GTG TTT AAC GGT TTT AGC TTT TTA TAA TAC CCT TGT GAG
   GGG GTC TTT CAC AAA TTG CCA AAA TCG AAA AAT ATT ATG GGA ACA CTC

                                              >Aha2
                                                |
         1210          1220          1230        | 1240          1250
           *             *             *         |  *             *
   AGC CCA TTC CCA CCA TTC TAC CTG AGG CCA GGA CGT CTG GGG TGT GGG
   TCG GGT AAG GGT GGT AAG ATG GAC TCC GGT CCT GCA GAC CCC ACA CCC

         1260          1270          1280          1290
           *             *             *             *
   GAT TGG TGG GTC TAT GTT CCC CAG GAT TCA GCT ATT CTG GAA GAT CAG
   CTA ACC ACC CAG ATA CAA GGG GTC CTA AGT CGA TAA GAC CTT CTA GTC

         1300          1310          1320          1330          1340
           *             *             *             *             *
   CAC CCT AAG AGA TGG GAC TAG GAC CTG AGC CTG GTC CTG GCC GTC CCT
   GTG GGA TTC TCT ACC CTG ATC CTG GAC TCG GAC CAG GAC CGG CAG GGA

         1350          1360          1370          1380          1390
           *             *             *             *             *
   AAG CAT GTG TCC CAG GAG CAG GAC CTA CTA GGA GAG GGG GGC CAA GGT
   TTC GTA CAC AGG GTC CTC GTC CTG GAT GAT CCT CTC CCC CCG GTT CCA

         1400          1410          1420          1430          1440
           *             *             *             *             *
   CCT GCT CAA CTC TAC CCC TGC TCC CAT TCC TCC CTC CGG CCA TAC TGC
   GGA CGA GTT GAG ATG GGG ACG AGG GTA AGG AGG GAG GCC GGT ATG ACG
```

Figure 3 cont.

```
                1450          1460          1470         1480          1490
                 *             *             *            *             *
          CTT TGC AGT TGG ACT CTC AGG GAT TCT GGG CTT GGG GTG TGG GGT GGG
          GAA ACG TCA ACC TGA GAG TCC CTA AGA CCC GAA CCC CAC ACC CCA CCC


             1500          1510          1520         1530
              *             *             *            *
          GTG GAG TCG CAG ACC AGA GCT GTC TGA ACT CAC GTG TCA GAA GCC TCC
          CAC CTC AGC GTC TGG TCT CGA CAG ACT TGA GTG CAC AGT CTT CGG AGG


          1540      1550          1560          1570          1580
            *        *             x             *             *
          AAG CCT GCC TCC CAA GGT CCT CTC AGT TCT CTC CCT TCC TCT CTC CTT
          TTC GGA CGG AGG GTT CCA GGA GAG TCA AGA GAG GGA AGG AGA GAG GAA


            1590         1600          1610          1620         1630
             *            *             *             *            *
          ATA GAC ACT TGC TCC CAA CCC ATT CAC TAC AGG TGA AGG CTC TCA CCC
          TAT CTG TGA ACG AGG GTT GGG TAA GTG ATG TCC ACT TCC GAG AGT GGG


             1640         1650          1660         1670          1680
              *            *             *            *             *
          ATC CCT GGG GGC CTT GGG TGA GTG GCC TGC TAA GGC TCC TCC TTG CCC
          TAG GGA CCC CCG GAA CCC ACT CAC CGG ACG ATT CCG AGG AGG AAC GGG


              1690         1700          1710          1720        1730
               *            *             *             *          ¿   *
          AGA CTA CAG GGC TTA GGA CTT GGT TTG TTA TAT CAG GGA AAA GGA GTA
          TCT GAT GTC CCG AAT CCT GAA CCA AAC AAT ATA GTC CCT TTT CCT CAT


            1740         1750          1760         1770
             *            *             *            *
          GGG AGT TCA TCT GGA GGG TTC TAA GTG GGA GAA GGA CTA TCA ACA CCA
          CCC TCA AGT AGA CCT CCC AAG ATT CAC CCT CTT CCT GAT AGT TGT GGT


                               >BamH1
                                |
         1780          1790    |1800           1810          1820
           *            *      |  *              *            *
          CTA GGA ATC CCA GAG GTG GAT CCT CCC TCA TGG CTC TGG CAC AGT GTA
          GAT CCT TAG GGT CTC CAC CTA GGA GGG AGT ACC GAG ACC GTG TCA CAT


          1830          1840          1850         1860          1870
            *             x             *            *             *
          ATC CAG GGG TGT AGA TGG GGG AAC TGT GAA TAC TTG AAC TCT GTT CCC
          TAG GTC CCC ACA TCT ACC CCC TTG ACA CTT ATG AAC TTG AGA CAA GGG


             1880         1890          1900         1910          1920
              *            *             *            *             *
          CCA CCC TCC ATG CTC CTC ACC TGT CTA GGT CTC CTC AGG GTG GGG GGT
          GGT GGG AGG TAC GAG GAG TGG ACA GAT CCA GAG GAG TCC CAC CCC CCA


            1930         1940          1950         1960          1970
             *            *             *            *             *
          GAC AGT GCC TTC TCT ATT GGC ACA GCC TAG GGT CTT GGG GGT CAG GGG
          CTG TCA CGG AAG AGA TAA CCG TGT CGG ATC CCA GAA CCC CCA GTC CCC


            1980         1990          2000         2010
             x            *             *            *
          GGA GAA GTT CTT GAT TCA GCC AAA TGC AGG GAG GGG AGG CAG ATG GAG
          CCT CTT CAA GAA CTA AGT CGG TTT ACG TCC CTC CCC TCC GTC TAC CTC
```

Figure 3 cont.

```
        2020            2030            2040            2050            2060
          *               *               *               *               *
        CCC ATA GGC CAC CCC CTA TCC TCT GAG TGT TTG GAA ATA AAC TGT GCA
        GGG TAT CCG GTG GGG GAT AGG AGA CTC ACA AAC CTT TAT TTG ACA CGT

        2070            2080            2090
          *               *               *
        ATC CCC TCA AAA AAA AAA CGG AGA TCC
        TAG GGG AGT TTT TTT TTT GCC TCT AGG
```
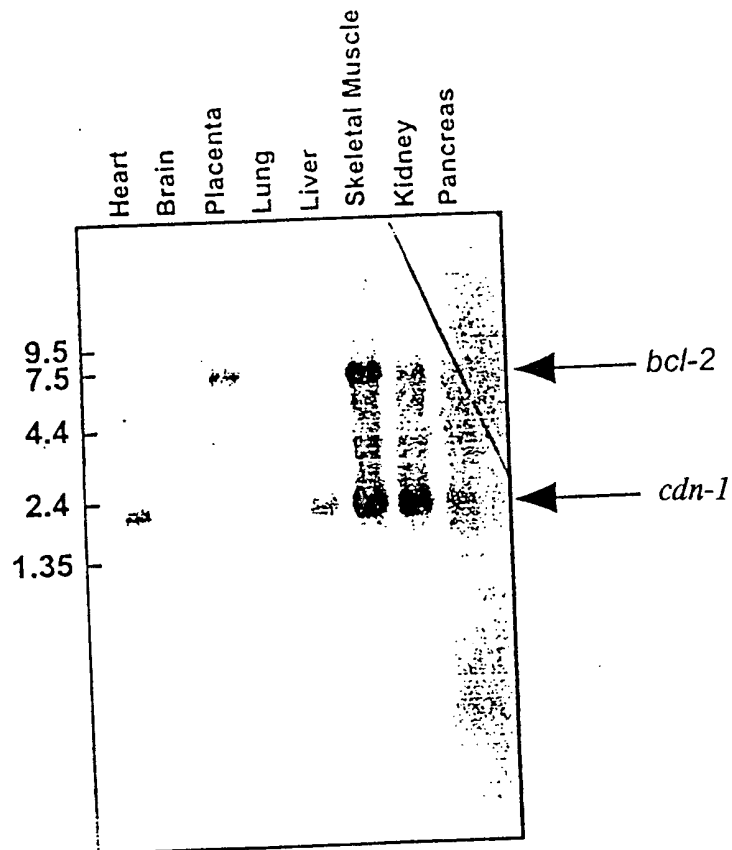
Figure 4

Multiple Tissue Northern
bcl-2 and cdn-1 hybridization

Random primed. Klenow-labeled fragments of
bcl-2 and cdn-1 clones were hybridized to a multiple
human tissue Northern blot (Clontech 7760-1), at a
final concentration of 1×10^6 cpm/ml for each probe.
Blot was washed at high stringency.

Figure 5   cdn-2 gene sequence

```
          10          20          30          40          50          60
           *           *           *           *           *           *
TTT TAA TAT AAA TTA ATG TGC TCT ATT TAT AGA GAC AAT ACA TGA AAT ATA CTT AAT AAA
AAA ATT ATA TTT AAT TAC ACG AGA TAA ATA TCT CTG TTA TGT ACT TTA TAT GAA TTA TTT

          70          80          90         100         110         120
           *           *           *           *           *           *
AAT TCA AAT GTT ATA GAA CTG AAA AAG ATG AAA AGT AAA AAC AAC CTA TTC CCC AGA GGT
TTA AGT TTA CAA TAT CTT GAC TTT TTC TAC TTT TCA TTT TTG TTG GAT AAG GGG TCT CCA

         130         140         150         160         170         180
           *           *           *           *           *           *
AGC CAC TGT CCA TAG TTT CTA TTT TAG ATT CTT TCC TTT ATA CAA GAT TAT TAT AGC TTC
TCG GTG ACA GGT ATC AAA GAT AAA ATC TAA GAA AGG AAA TAT GTT CTA ATA ATA TCG AAG

         190         200         210         220         230         240
           *           *           *           *           *           *
TAT TTT TTG GTG TAT GAA CTG TAG TCC TAG AGG ATT TTA TTA GTT ATG AGT TCT ATA ACT
ATA AAA AAC CAC ATA CTT GAC ATC AGG ATC TCC TAA AAT AAT CAA TAC TCA AGA TAT TGA

         250         260         270         280         290         300
           *           *           *           *           *           *
AAG ATC CAT CAT CTT AGT TGC TAA GAA CGT AGA TAC TGA GAA CAT CAT TTA AAA AAA CAT
TTC TAG GTA GTA GAA TCA ACG ATT CTT GCA TCT ATG ACT CTT GTA GTA AAT TTT TTT GTA

         310         320         330         340         350         360
           *           *           *           *           *           *
TTT TGG CTG GCA CCT CAT GAT CAC TGG AGT CTC GCG GGT CCC TCA GGC TGC ACA GGG ACA
AAA ACC GAC CGT GGA GTA CTA GTG ACC TCA GAG CGC CCA GGG AGT CCG ACG TGT CCC TGT

         370         380         390         400         410         420
           *           *           *           *           *           *
AGT AAA GGC TAC ATC CAG ATG CTG GGA ATG CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC
TCA TTT CCG ATG TAG GTC TAC GAC CCT TAC GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG

         430         440         450         460         470         480
           *           *           *           *           *           *
CCA CTC AGC CCC TGG GAG CAG CAG CCG CCA GCC CCT CGG GAC CTC CAT CTC CAC CCT GCT
GGT GAG TCG GGG ACC CTC GTC GTC GGC GGT CGG GGA GCC CTG GAG GTA GAG GTG GGA CGA

                              >BamHI
         490         500|        510         520         530         540
           *           * |         *           *           *           *
GAG CCA CCC GGG TTG GGC CAG GAT CCC GGC AGG CTG ATC CCG TCC TCC ACT GAG ACC TGA
CTC GGT GGG CCC AAC CCG GTC CTA GGG CCG TCC GAC TAG GGC AGG AGG TGA CTC TGG ACT

         550         560         570         580         590         600
           *           *           *           *           *           *
AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA GAG CCT GCC CTG
TTT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG CCT CTC GGA CGG GAC
     M   A   S   G   Q   G   P   G   P   P   R   Q   E   C   G   E - P   A   L>

         610         620         630         640         650         660
           *           *           *           *           *           *
CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT
GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG TGT CTC CTC CAA AAG GCG TCG ATG CAA
 P   S   A   S   E   E   Q   V   A   Q   D   T   E   E   V   F   R   S   Y   V>

         670         680         690         700         710         720
           *           *           *           *           *           *
TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG
AAA ATG GTG GTA GTC GTC CTT GTC CTC CGA CTT CCC CGC CGA CGG GGA CGG CTG GGT CTC
 F   Y   H   H   Q   Q   E   Q   E   A   E   G   A   A   A   P   A   D   P   E>
```

Figure 5 cont.

```
                                          >Nco1
        730         740         750     |     760         770         780
         *           *           *     |      *           *           *
    ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC
    TAC CAG TGG AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG CGG
     M   V   T   L   P   L   Q   P   S   S   T   M   G   Q   V  .G   R   Q   L   A>


        790         800         810         820         830         840
         *           *           *           *           *           *
    ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC
    TAG TAA CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC TGG TAC AAC GTC GTG
     I   I   G   D   D  .I   N   R   R   Y   D   S   E   F   Q   T   M   L   Q  'H>


       >Pst1
        |      850         860         870        880         890         900
        |       *           *           *          *           *           *
    CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT
    GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG AAG TGG TTC TAA CGG AGG TCG GAC AAA
     L   Q   P   T   A   E   N   A   Y   E   Y   F   T   K   I   A   S   S   L   F>


        910         920         930         940         950         960
         *           *           *           *           *           *
    GAG AGT GGC ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC
    CTC TCA CCG TAG TTA ACC CCG GCA CAC CAC CGA GAA GAC CCG AAG TCG ATG GCA GAC CGG
     E   S   G   I   N   W   G   R   V   V   A   L   L   G   F   S   Y   R   L   A>


        970         980         990         1000        1010        1020
         *           *           *           *           *           *
    CTA CAC ATC TAC CAG CGT GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG
    GAT GTG TAG ATG GTC GCA CCG GAC TGA CCG AAG GAC CCG GTC CAC TGG GCG AAA CAC CAC
     L   H   I  .Y   Q   R   G   L   T   G   F   L   G   Q   V   T   R   F   V   V>


        1030        1040        1050        1060        1070        1080
         *           *           *           *           *           *
    GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA
    CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC CCA CCG ACC CAC CGT
     D   F   M   L   H   H   C   I   A   R   W   I   A   Q   R   G   G   W   V   A>


        1090        1100        1110        1120        1130        1140
         *           *           *           *           *           *
    GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG
    CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG CAC GAC CAC CAA GAC CCA CAC CAA GAC
     A   L   N   L   G   N   G   P   I   L   N   V   L   V   V   L   G   V   V   L>


        1150       1160         1170        1180        1190        1200
         *           *           *           *           *           *
    TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTC CCA AGG GTG CCT TTG GGG
    AAC CCG GTC AAA CAC CAT GCT TCT AAG AAG TTT AGT ACT GAG GGT TCC CAC GGA AAC CCC
     L   G   Q   F   V   V   R   R   F   F   K   S   *>


        1210        1220        1230        1240        1250        1260
         *           *           *           *           *           *
    TCC CAG TTC AGA CCC CTG CCT GGA CTT AAG CGA AGT CTT TGC CTT CTC TGC TCC TTG CAG
    AGG GTC AAG TCT GGG GAC GGA CCT GAA TTC GCT TCA GAA ACG GAA GAG ACG AGG AAC GTC


                                     >Hind3
        1270        1280          |
         *           *            |
    GGT CCC CCC TCA AGA GTA CAG AAG CTT
    CCA GGG GGG AGT TCT CAT GTC TTC GAA
```

Figure 6   Amino acid sequences of cdn-1, cdn-2, and bcl-2 family proteins

```
cdn1      masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyrhqqeeaegvaapadpemvt
cdn2      masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyHhqqeeaegAaapadpemvt
bcl2      mahagrtgyDNREIVMKYIHYKLSQRGYEWdagdvgaapapgifsspghtaasrdpvartsplqtpaapgaa
bax                 mdgsgeqprggpptsseqimktgalllggfiqdragrmggeap
bcl-x     msqSNRELIVDFLSYKLSQKGYSWsqfsdveenrteapegtesemetpsaingnpswhladspavngatghssl
mcl-1     ...(+123 aa)eldgyepeplgkrpavlplelvgesGnntstdgslpstpppaeeeedelyrqsleiisrylreqatgakdtk
A1                                                              maeselmhihslaehylqyvlq
bhrf                                                              megeeliyhniineilvgy
LMW5-HL
ced9      mtrctadnsltnpayrrrtmatgemkeflgikgteptdfginsdaqdlpspsrqastrmsigesidgkindweeprlDIEGFVVDYFTHRIRQNGMEWfgapg
```

```
cdn1      lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH
cdn2      lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGI-NWGRVVALLGFSYRLALHIYQRGLTGFLGQVTRFVVDFMLHH
bcl2      agpalspvppVVHLTLRQAGDDFSRRYRRDFAEMSRQLHLtpftargRFATVVEELFRDGV-NWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEY-LNR
bax       elaldpvpqdastkklseclkrigdeldsnmelqrmiaavdtdsprevFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDF-LRE
bcl-x     darevipma-AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGV-NWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATY-LND
mcl-1     pmgrsgatsrkalETLRRVGDGVQRNHETVFQGMLRKLDIKNEDDVKSLSRVMIHVFSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITD-VLVR
A1        vpafesapsgqacrvlqrvafsvqkeveknlksylddfhvesidtarlifNQVMEKEFEDGIINWGRIVTIFAFGVLLKKLpqeialdvcaykqvssfvaefl
bhrf      etplrlspedtvvlryhvlleeliernsetffetwnrfithtehvdldfnsvfleifhD-LINWGRICGFIVFSARMAKYCKDANn-HLESTVITTAYNF-SEG
LMW5-HL   ikyymndihelspyqqgikkiltyydeclnkqvtitfsltnaqelktQFTGVVTELFKrgdpslgralawmawcmhacrtlccnqstpYYvvdlsvrgmleaM-
ced9      lpcgvqpehemmrvmgtifekkhaenfetfceqLlavpriefslyqdvvrtvgnaqtdqcpMSYGRLIGLISFGGFVAAKMmesvelgqgvrnlfvytslfIKT
```

```
cdn1      CIAR--WIA--QR-GGWVAALNLGngpilnvlvvlgvvllggfvvrrffks
cdn2      CIAR--WIA--QR-GGWVAALNLGngpilnvlvvlgvvllggfvvrrffks
bcl2      HLHT--WI--QDNGGWDAFVELYgpsmrplfdfswlslktllslalvgacitlgaylghk
bax       RLIG--WI--QDQGGWDGLLSYFgtpwtgtvtifvagvltasltiwkkmg
bcl-x     HLEP--WI--QENGGWDTFVELYgnnaaaesrkgqerfnrwfltgmtvagvvllgelfsrk
mcl-1     TKRD--WLVKQ--RGWDGFVEFFhvedleggirnvllafagvagvagvgaglaylir
A1        MNNTGEWI-RQ-NGGWEdgfikkfepksgwltflqmtggiwemlfllk
bhrf      -LDG--WIHQQ--GGWstliednipgsrrfswtlflaglitlsllvicsylfisrgrh
LMW5-HL   KHNLLPWMISH--GGQEEFLAFslhsqiysvifnikyfislekfcnhhflmscvqllrkcnli
ced9      -RIRNNWKE-H-NRSWDDFMTLgkqmkedyeraeaekvgrrkqnrrwsmigagvtagaigivgvvvcgrmmfslk
```

SEQUENCE IDENTITY:

cdn1/cdn2 = 97%

Figure 7   cdn-3 enzyme annotated sequence

```
                                                                         80
GAATTCTCCT AATTAGTTAA ACAACCTTGA ACAACTTCTT TCACTTCTCT CAGTCTCACT TTCTCACTCA AAAATCCTCA

                                                                        160
ATAATTTGTA AGACTTCGCT AATAATCTAC GACTCTACAA GAGGCAATAG CCTACTCTGG ACAGAGAGCA GGCTTTGGAA

                                                                        240
ACACACAAGA CTGCGTTTAG ATTCCTCCAC TCCACCCACT GTGTCACTTG GCCAACCTTC TTCACTTCTC TAAACCCCCA

                                                                        320
TCTGTGTATC TGTACAGCAA TGAATGAATG ACTATGTCCA GCCAAGCTAT CCAAACTCCA GGTTAAAATA TTGCCTTCCG

                                                                        400
TTTTTTACTA AATTGTTCAA GCCCATCACA TTCTAGCAGA AAAAGCCTAC TCTCTCTTTC TTAAGGTCAT TGTGTGCATG

                                                                        480
TGTTTTCCAG GAACTCTATG GGTTTCTCAA CCCAAATTCA CCCTGCCCTT GACCAAATGG CTCACCACCT TCACCGATCC

                                                                        560
TGCTCTGATG ACACAOCCTG CACTCACCAT CTGCCCCTGC ACCTACAATG CACTTCTGAC TGCCCATTAG CTGCGGGATA

                                                                        640
CCACATCCCC ACCAATCTCA CACATCTTCT OTCACACTCC ACCCCCAACC ATTCCTTCTC AAATCATAAT CCCTTACCAC

                                                                        720
GACACCTACC TGCACCACCC ATGACACAAA CACCACCCCT TCCCTACAAT CTCACCCACT ATCTTCACTC TGACCAACTA

                                                                        800
CTCTAGTGGC AGGCGGGCCC TTCCTTTTCA AGACACTTCT GCCATCACAT CCTTTCACAA ACACATCCCT CCCCACCCTG

                                                                        880
CCTCTTCTCC AGGTCTCCAC ACTCAAAAGT AACACACGCAT TTGCTAACCC ATATTTCAAA AACTTTCCTT ATACCTTCAT

                                                                        960
CTCACGACAA CACGTCCCTG CTTAACACCC TTATCTTTCT CTCACTGCTA TTTTTTTTTC CCCTGACCTT CCAACGCCTA

                                                                       1040
CTCTACTTTC TCCCTCCCTA CCTGAACAAA AGTCAACTTC AAATAATTTC AACTACCCCT TTTTGTCCGC ACCCCATTTG

                                                                       1120
ATTTTTTACCT TACCCAGAGC CCTTAATTTGT CCATCTCACC ATAGCACTAC CTTCCACCAC CTGAGCCACA ATACATTCTT

                                                                       1200
TAAAGACTGA CACTCCCTCC CATTCCAATA ACAACCACAC TCACAGCAAA GCTTCCCTCT CCTGTCTGGA GACTGACCCA

                                                                       1280
TGGTACAAAA TTTCCACACT TCCTTACCTC TTCATCACTT CAAAAATCTA TTTATTCATT TATGCATTTA ATTTTCCCTA

                                                                       1360
TCTAAGCCAG CCATACTCAA ACATTTCTC TAAACCCCCA ACACCCATCA TAAATATGTT ACGCTCTCCA GCCCACTTAC

                                                                       1440
ACTTTTCTCA TGCATTCTTT TTCTGCTCCC TCTTTGTATT ATTTTGTTTA CACTCCTTTA AAAACCTAAA AAAACACATTC

                                                                       1520
ATCACTCGAG TCTCACCCGT CCCTCCCCCC ACACACCCAC AACCAAACCC CACATCCACA TACCACAAAT CCCACTCACCC

                                                                       1600
CCGTTCCTCC AAGCTCCCCT CCCACTCACC CCCTCCCACC ACCAGCCTCC ACCCCCTTCC GACCTTCAAC TCCACCCTCC
```

Figure 7 cont.

TCACCCACGC CGGTTGA ● AGCATCCCTG CAGGCTCACA CTGTCCTCCA CTGAA ● G AAAA ATG CCA TCC CGG
                                                                           M   A   S   G>

1680
CAA CCC CTA CCC CCT CCC ACC CAC CAC TGC CCA AAG CCT GCC CTC CCC TCT GCT TCT CAG CAG CAG
Q   C   P   P   P   P   R   D   B   C   O   K   F   A   L   P   S   A   S   E   E   Q>

1760
CTA CCC CAG GAC ATG CAG CCG TTT TCC CCA CCT ACC TTT TTT ACC ACC ATC AGC AGC AAC ACG ACG
V   A   Q   D   M   E   G   F   S   A   A   T   F   F   T   T   I   S   R   N   R   R>

1840
CTG AAG CCG CCG CCG CCC CTC CCG ACC CAG ACA TCG TCA CCT TCC CCC TCC AAC CTA CCA CCA CCA
L   K   G   R   P   P   L   P   T   Q   R   M   S   P   C   P   S   N   L   A   A   P>

1920
TCG CCC ACC TCC CAC CCC ACC TCG CCA TCA CCA CGA CCA CAT CAA CTG CCA CTA TCA CTTCCGAGT
M   G   R   W   D   G   S   S   P   S   P   G   R   Q   P   A   L   *>

2000
TCCTGACCAT GCTCCAGCAC CTGCAGCCCA CCGCAGAGAA CGGCTACGAG TACTTCACCA AGATCCCCTC CACCCTCTTT

2080
CACAGTCGCA TCAACCGGGG CCGTGTGGTG GCTCTCCTGG GCTTCGGCTA CCGTCTCGTC CTACATGTCT ACCAGCACGG

2160
CTTCACTCGC TTCCTCGGCC TGGTCACCCG CTTCGGTCGTC TTCATGCTGC AACAAGGCAT CGCCCGGTGG ATCTCCCAGA

2240
CGGCGGGCTG GGTCGCACCC CTCGACTTCG GCAATAGTCC CATCCTGAAC GTCCTGGTCG TTGTCGGTGT GGTTCTGCTG

2320
CGCCABTTTG TCGTAAGAAG ATTCTTCAAA TCATGACTCC CAGGGGTCTC CTTTGGGGTC CCAGCTGTGA CGCCTGCCTG

2400
CACCTAAGCC AAGTCTTTGC CTTCCCCACT CCCTTGCAGG GCTCACCCTT CAAAAGTACA CAAGCTCTAG CAAGTCTGCA

2480
CCCCCGGCTGC CCAGGGCCCC TGGGTGGGGG CCACTCACGC TGCCGAGGCA CCTCAACATT CCACCCTCCT ACTCGCCCCT

2560
CTCTCTCGCC CCAGGGCCTG TCCCCTCCTC CCTTGGCTCT CTGCGAACTC CTTACTCTTG TCTCCTACGC GCTCCACGACG

2640
CTGATAACTT GGGCAAGCAA GAGACTCGGA GCCACTCCTC CCCAGTAAGT CTTTAACCGT TTTAGCTTTT TATAATACCC

2720
TTGCCAGACC CCATTCCCAC CATTCTACCC AAGGCCGGGA TGTCTCGGGT GTCCGGGTTG GTCCGTCCTA ACCTACGTGC

2800
CCCACCATTC AACTATTCTG CAAGATCAGA GCCTAAGACC TACCACTTCA TCCTCCTCCT CCCCCTCCCT AAGCATCATG

2880
TGTCCCACGA CCACCACTCA CTGCGACACG CGACCAAGGT CCTACCCACC TCTCCCCGTG CCCCCATTCC TCCTCCGGCC

2960
ATACTCCCTT TCCAGTTGGA CTCTCACCGA TTCTCCGCTT GGGGTGTGGG CCGGCGTGGA CTAACAGGCC ACAACTGTCT

3040
CAACTTATGT CTCACAAGCC TCCAAGCCTG CCTCCCAAGG TCCTCTTCAGG TCTCTCCCTT CCTCTCTCCT CATACATACT

3120
TCCTCCCAAC CCATTCACTA CAGGTGAAGG CCCCTCACCCA TCCCTCCCGG CCTTGGGTGA CTGATGCGCT AAGGGCCCTC

Figure 7 cont.

```
                                                                        00
CCTGCGCAGA CTACAGCGCT TGGTTTACGG CTTGCATTCT TATTTCACGC ATAAGCAGTA GGCAGTTCAT CTGGCAAGGTT

                                                             3280
CTAACTGGCA CAAGGACTAT CAACAGCAGA GGAATCCGAG AGGTGGGATC CTCCCTCATG GGTCTGGCAG AGTGTAATCC

                                                             3360
AGGGGTGGAG ATAGGGAACT GTGAAATAGCT GAAGTCTGTC GGGGGACCGT CCAGGCTCCT CACGTTTCTG GGTGTGTGCT

                                                             3440
CAGTGTGGGG GTGAGAGTAG CTTGTGTATG GGGGCACAGCC TAGGGGTGTTG GGGGTGAAGG GGGAGGAAGTT GTTGATTGAG

                                                             3520
GGAAATGGAG GGAGGGGAGGG GAGAAGGAGG CGACAGGGGCCA GTGGGGTATGG TGTGAGTGTTT TGGAAATAAA GTGTGGGCAAGTC

                                                             3600
GGGATGAAAAA AAAAAAGGAG AAAAAAATGT AAAAAAGGATG CTTAGGGTGTA AGGTACTTAT AGGGGGCATAA AGAGGAGGGACT

                                                             3680
GTTAATGGAG AGAAAGATAG AGTTAGAGAGG AAGAAATAAG TTGTGTGGGAG GGAGGGGTGGGC TGAGAGGGGTGT AAGTGGGAGGGGA

                                                             3760
GTTTGGGAGA GGGAAGTGGGG AAGATGGATTT GAGTGGGAGGGA GTTGGAGGGACG AGGGGTGGGACA AGAGAGGGGAAG ATGTTATGTG

                                                             3840
TAGAGGAAAAT TTAAAAAAAAA GAAAAAAAGCT AGGGGGGGGACAG GTGTGGGAGTG GTAGGGTAGTG GGGAGGGGCTAAA GGTGGGGAAGAA

                                                             3920
TGGTTGAAGGGG GAGGGGATTTA GTTTGAGGGTT GGGAGTGAGGGCT ATGGTTGGGCAG GAGTGGCAGTG GAGAGTGGGGGT GAGTGAGTGA

                                                             4000
GAGGGTGTGGT GAAATATAAA GAAGGGAAGGAA GTTGTAGTTT TGAATAGGGGG AAGAGGGGTGGA GTGGAGTTAG GGAGAAGGGATA

                                                             4080
TTGTGTATTT GAAAATAGGGT AGAAGAGGAGGGG ATATGGAAGTGG TTGGGGGGGGAAAA GAAGGGAATGGA TAAGGGTTGGGA GGTGGGAGGAGGGT

                                                             4160
AGGGTTAAAATA GGGGTTGGATTTGG ATGATTAGGGAC ATTGGAATGGTA TGTATGGGAAAA TATTAGGGATGT AGGGGGAGGGAAAA TTTGTGTAAA

                                                             4240
TATTTATGTGGT GGGAGTTTTTTA AAGTTGGGGGGGG AGGGGGGAAAAG GAGTAGGTATG GGTTGGGGGGTGG GTGGGGTGTGGGA GGGAGTGGGGGAG

                                                             4320
GTGAGGGGAAAT GTATGGAGGGGGA AAATGTGGGGGG AAGTGTGGGGGAA ATTGGGGTTGGA TGGGGAGGGTAT GGGTTTGGGGGGA GTGGGTAGGGGAA

                                                             4400
TGATTTGGGGAG AGATAGGGTTAA TGGTGAATTGGG GGGGGAGTGGTTT GGTTGGAGGGGAGG TTTGGGGTGGGGG GAGGGAAGGGATG AGTGAGGAGTGG

                                                             4480
AGGTGTTGGGG ACTTGAGGGTGG GGGGTGTTAGGGG GGAAGGGAGGGGGGA AATGGGAGGTGGT TGTGGTGGAAAC GGGAAGGGTTGG TAGAAAGGGAGGGA

                                                             4560
GGGTGTGGGGGG ATGGGGAAGGGAT GTGGGGGTGGGAT GGGAGGGTGGAA GTTTAGTTGGGA GGTGGGGGGGGGGT TGGGGGGGTTTG GGAAGGGGTGGGTT

                                                             4640
TGTTTTTGGTT GGTTGGAGTGGGG AGTGGGGGGGGTG GGGTTGGGGGTGG GGGGGGGGGGGGGG AGGGGTTTAGT GAGTGTGTGTTCT GTTGTGGGGGGAAA

                                                             4720
GGTGTGTGTGTA TAGTTTAGTGGGA GTTTGTGGGAG GGGGGTGGATGT TTGGTGTTTGT GGTAAAGGAAAT AAGTAGGAGTGG TTTTAAAGGAAAA

                                                             4800
TATTTGGAGGGGG GGGGGGTGGGGGGT GGTTGAGGGGGTGG TGTTAATGGGAG GGGTTTGGGGAA GGGGGAAGGGGGGA GGTGGATGGAT GGGGGTGGGGGGGGA
```

Figure 7 cont.

Figure 7 cont.

```
                                                          4880
CTTTCAGACC ATCATCGGCA ACATGGTGAA ACCCCATCTC TACTGAAAAC ACAAAAATTA CCTCGCTCTC GTGGCGGGCA

                                                          4960
CCTCTAGTCC CAGCTACTCC GGAGGCTGAG GCAGGAGAAT CCCTTGAGCC TGGGAGGCGG AGGTTGCACT GAGCCGAGAT

                                                          5040
CACGGCACTG CACTCCAGCC TGGGGACAGA GCGAGACTCC ATCTCAAAAA AAAGAAAAAA TAAATAGTTG AAATAAAGAC

                                                          5120
TGCACATAAA GACAAAAAAA AAGTTTATAA AGTTAAAAAA TAAAATAAAA AACACGCTCC AGGCTGGATT GGGCCCAGAG

                                                          5200
GCTGTAGGAC ACAGACCCCC AGGCAATGAC TTCATAAATC GGCATGTTAA TCAGCCTCAG CTGGGAATTT GGGGAGGGGA

                                                          5280
CTCATTTTAA AACAGTTTCC TGGATTCTAA CCCAACCCAG AAAATCAGAC TCTTTGAGCT AAATTCTTAA GCTCCCTGGT

                                                          5360
GATGATGATG GAAGCAGTTT ATGGCTCACC CCAGACTACC GTCTGAAAGA CCTGCCACAT GGCTCTCTCT CCAGCCTCCC

CTTCTCCTGC ATCCCCAGG GAGAATTC
```

Figure 8

Wil-2 transformants 0.1% FBS

Legend:
- pcdna average
- bcl-2 average
- cdn-1 rbss average
- wil-2 wt average
- cdn 1Δ2 average
- cdn1-112 average
- bax average
- baxΔ3 average
- bcl-x average

Figure 9

Response of WIL-2 Transformants to anti-Fas-Induced Apoptosis

50 ng/mL anti-FAS

Proportion of Cells Surviving
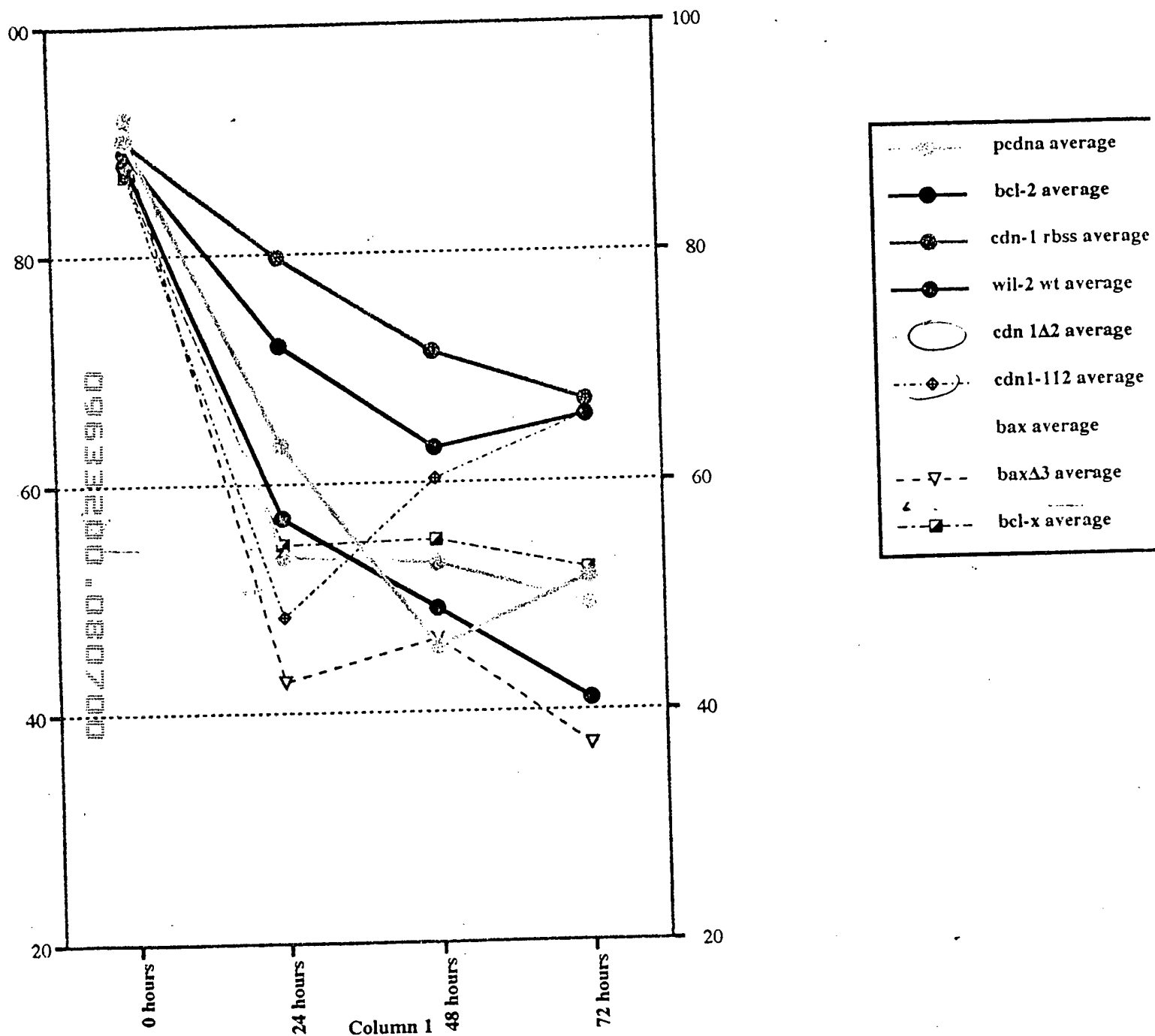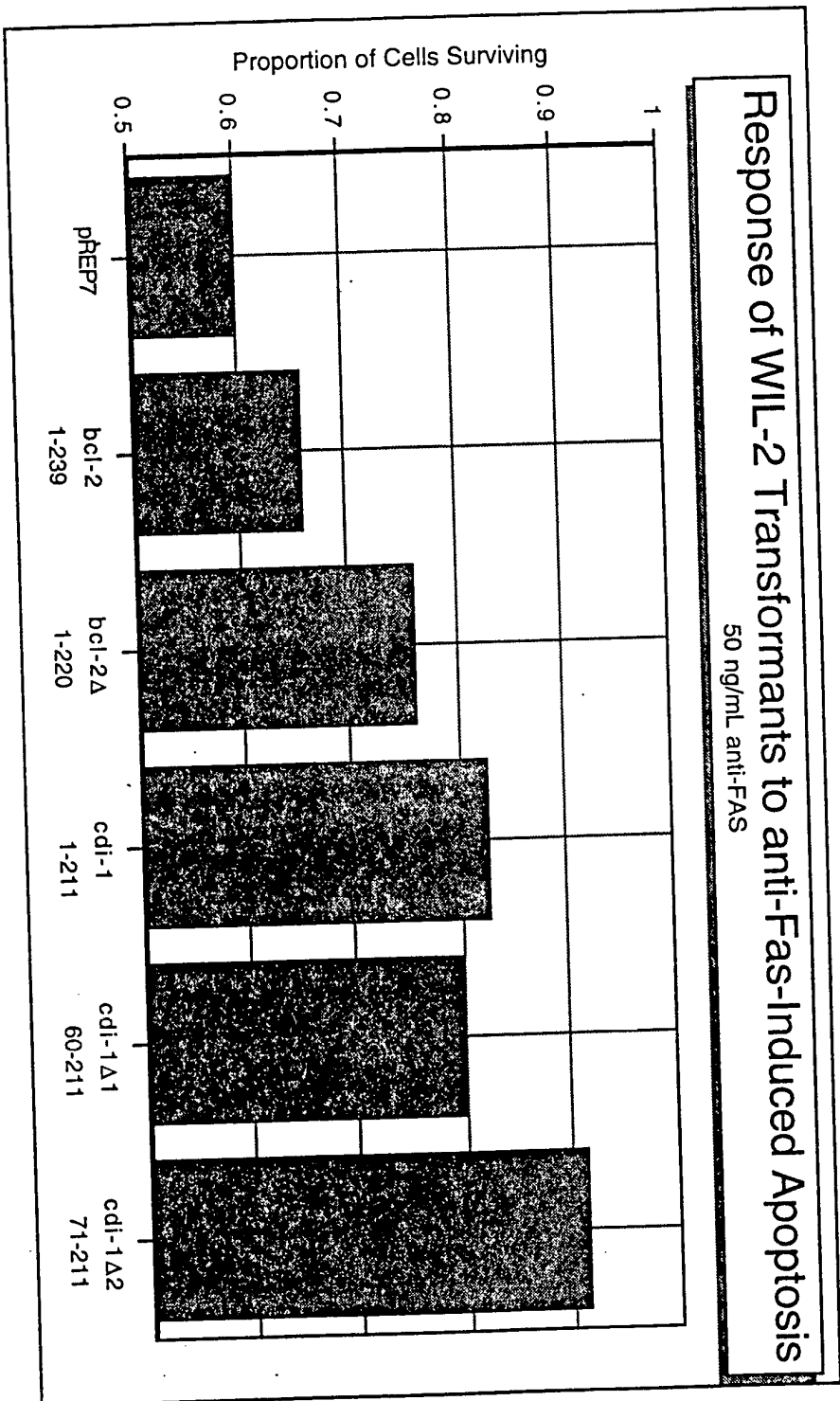
Figure 10

F15.12 transformants - IL-3

Legend:
- pcdna average (□)
- bcl-2 average (◇)
- cdn-1 average (○)
- cdn-2 average (△)
- cdn 1Δ2 average (⊞)
- cdn1-112 average (◈)

X-axis: 26 hours, 50 hours, 74 hours, 98 hours

Y-axis: 0 to 100 (intervals of 25)
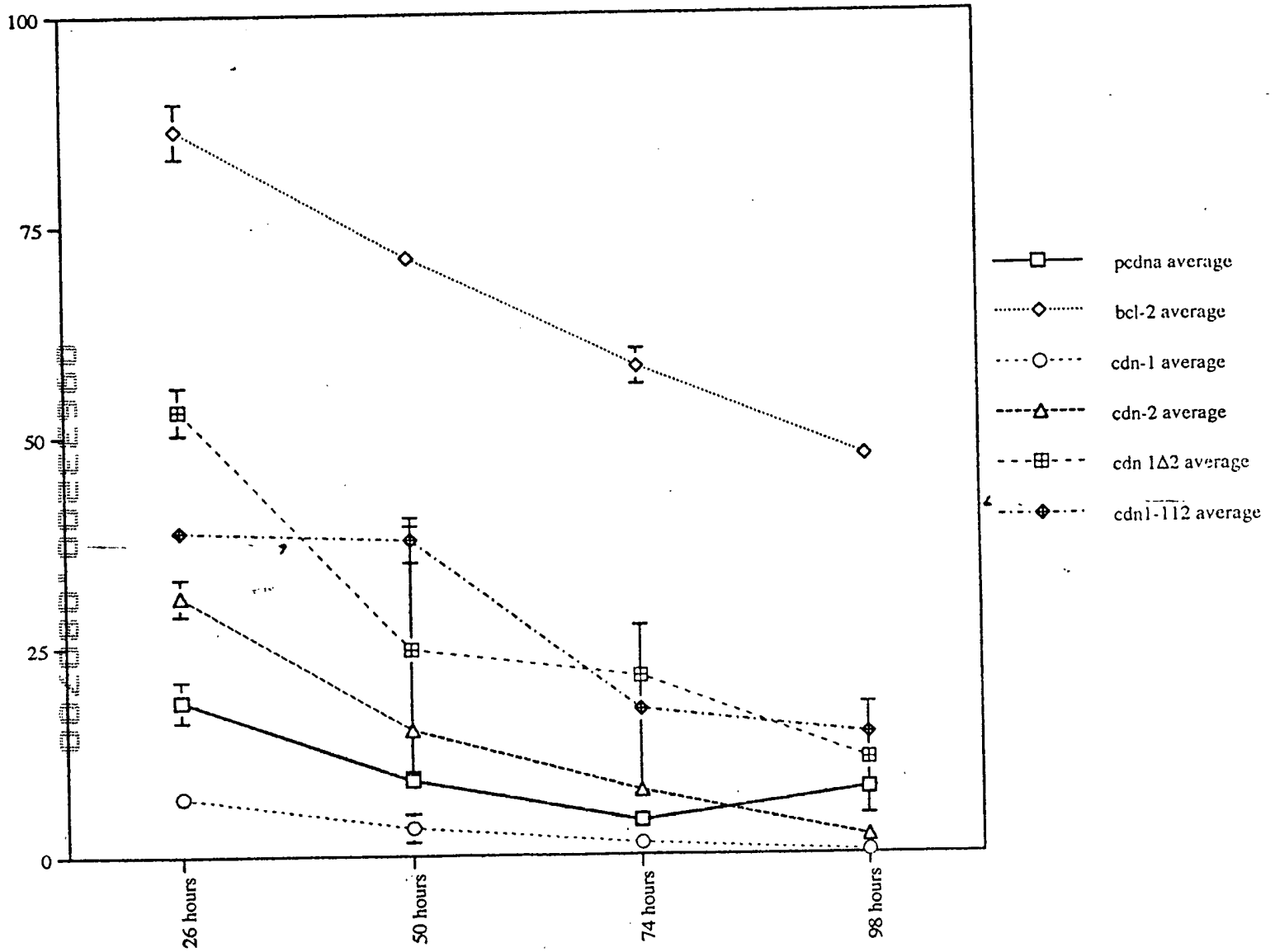
Figure 11   N-terminal methionine residues of cdn-1 derivatives

```
                    MASGQGPGPFRQECGEPALPSASEEQVAQDTEEVFRSYVFYRHQQEEAEGVAAPADPEMVT
                                                                           Δ1
                                                                           →

     Δ3
LPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGNWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH
  Δ2                             →
  →
CIARWIAQRGWVAALNLGNGPILNVLVVLGVVLLGQFVVRRFFKS
```